

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: TAKAHASHI, Tohru
SERIZAWA, Nobufusa
KOISHI, Ryuta
KAWASHIMA, Ichiro
- (ii) TITLE OF INVENTION: EXPRESSION SYSTEMS UTILIZING
AUTOLYZING FUSION PROTEINS
AND A NOVEL REDUCING POLYPEPTIDE
- (iii) NUMBER OF SEQUENCES: 19
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Frishhauf, Holtz, Goodman, Langer & Chick, P.C.
(B) STREET: 767 Third Avenue-25th Floor
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: United States
(F) ZIP: 10017-2023
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.24
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/500,635
(B) FILING DATE: 11-JUL-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-161053
(B) FILING DATE: 13-JUL-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-218392
(B) FILING DATE: 13-SEP-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: JP 6-303809
(B) FILING DATE: 07-DEC-1994
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Goodman, Herbert
(B) REGISTRATION NUMBER: 17081
(C) REFERENCE/DOCKET NUMBER: 950376/HG
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 319-4900
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1320 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double

03942347-042304

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Clover Yellow Vein Virus

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1320

(D) OTHER INFORMATION:

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 10..1311

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAG TTC CAA GGG AAA AGT AAG AGA ACA AGA CAA AAG TTG AAG TTC AGA	48
Lys Phe Gln Gly Lys Ser Lys Arg Thr Arg Gln Lys Leu Lys Phe Arg	
1 5 10 15	
GCG GCA AGA GAC ATG AAG GAT CGT TAT GAA GTG CAT GCC GAT GAG GGG	96
Ala Ala Arg Asp Met Lys Asp Arg Tyr Glu Val His Ala Asp Glu Gly	
20 25 30	
ACT TTA GTG GAA AAT TTT GGA ACT CGT TAT TCA AAG AAA GGC AAG ACA	144
Thr Leu Val Glu Asn Phe Gly Thr Arg Tyr Ser Lys Lys Gly Lys Thr	
35 40 45	
AAA GGT ACT GTT GTG GGT TTG GGT GCA AAA ACA AGA CGG TTC ACT AAC	192
Lys Gly Thr Val Val Gly Leu Gly Ala Lys Thr Arg Arg Phe Thr Asn	
50 55 60	
ATG TAT GGT TTT GAC CCC ACG GAG TAT TCA TTT GCT AGG TAT CTT GAT	240
Met Tyr Gly Phe Asp Pro Thr Glu Tyr Ser Phe Ala Arg Tyr Leu Asp	
65 70 75 80	
CCA ATC ACG GGT GCA ACA TTG GAT GAA ACC CCA ATT CAC AAT GTA AAT	288
Pro Ile Thr Gly Ala Thr Leu Asp Glu Thr Pro Ile His Asn Val Asn	
85 90 95	
TTG GTT GCT GAG CAT TTT GGC GAC ATA AGG CTT GAT ATG GTT GAC AAG	336
Leu Val Ala Glu His Phe Gly Asp Ile Arg Leu Asp Met Val Asp Lys	
100 105 110	
GAG TTA CTT GAC AAA CAG CAC TTA TAC CTC AAG AGA CCA ATA GAA TGT	384
Glu Leu Leu Asp Lys Gln His Leu Tyr Leu Lys Arg Pro Ile Glu Cys	
115 120 125	
TAC TTT GTA AAG GAT GCT GGT CAG AAG GTG ATG AGG ATT GAT CTA ACA	432
Tyr Phe Val Lys Asp Ala Gly Gln Lys Val Met Arg Ile Asp Leu Thr	
130 135 140	
CCC CAC AAC CCA TTG TTG GCA AGC GAT GTT AGC ACA ACC ATA ATG GGT	480
Pro His Asn Pro Leu Leu Ala Ser Asp Val Ser Thr Thr Ile Met Gly	
145 150 155 160	

TAT Tyr	CCT Pro	GAG Glu	AGA Arg	GAA Glu 165	GGT Gly	GAA Glu	CTC Leu	CGT Arg	CAA Gln 170	ACT Thr	GGA Gly	AAG Lys	GCA Ala	AGG Arg 175	TTA Leu	528
GTC Val	GAC Asp	CCA Pro	TCA Ser 180	GAG Glu	TTG Leu	CCC Pro	GCG Ala	CGG Arg 185	AAT Asn	GAG Glu	GAT Asp	ATT Ile 190	GAT Ala	GCA Ala	GAG Glu	576
TTT Phe	GAG Glu	AGT Ser 195	CTA Leu	AAT Asn	CGC Arg	ATA Ile	AGT Ser 200	GGT Gly	TTG Leu	CGC Arg	GAC Asp	TAT Tyr 205	AAT Asn	CCC Pro	ATT Ile	624
TCA Ser	CAA Gln 210	AAT Asn	GTT Val	TGC Cys	TTG Leu	CTA Leu 215	ACA Thr	AAT Asn	GAG Glu	TCA Ser	GAA Glu 220	GGC Gly	CAT His	AGA Arg	GAG Glu	672
AAG Lys 225	ATG Met	TTT Phe	GGA Gly	ATT Ile	GGA Gly 230	TAT Tyr	GGT Gly	TCA Ser	GTG Val	ATC Ile 235	ATT Ile	ACA Thr	AAT Asn	CAA Gln	CAT His 240	720
CTG Leu	TTC Phe	AGA Arg	AGG Arg	AAT Asn 245	AAT Asn	GGG Gly	GAG Glu	TTA Leu	TCA Ser 250	ATT Ile	CAA Gln	TCC Ser	AAG Lys	CAT His 255	GGC Gly	768
TAC Tyr	TTC Phe	AGA Arg	TGC Cys 260	CGC Arg	AAC Asn	ACC Thr	ACA Thr	AGC Ser 265	TTG Leu	AAG Lys	ATG Met	CTG Leu	CCT Pro 270	TTG Leu	GAG Glu	816
GGA Gly	CAT His	GAC Asp 275	ATT Ile	TTG Leu	TTG Leu	ATT Ile	CAG Gln 280	TTA Leu	CCA Pro	AGG Arg	GAC Asp	TTT Phe 285	CCA Pro	GTG Val	TTT Phe	864
CCA Pro	CAA Gln 290	AAG Lys	ATT Ile	CGC Arg	TTT Phe	AGG Arg 295	GAG Glu	CCA Pro	AGA Arg	GTG Val	GAT Asp 300	GAC Asp	AAA Lys	ATT Ile	GTT Val	912
TTG Leu 305	GTC Val	AGC Ser	ACA Thr	AAT Asn 310	TTC Phe	CAG Gln	GAA Glu	AAG Lys	AGT Ser	TCC Ser 315	TCG Ser	AGC Ser	ACG Thr	GTC Val	TCA Ser 320	960
GAG Glu	TCC Ser	AGT Ser	AAC Asn 325	ATT Ile	TCA Ser	AGA Arg	GTG Val	CAG Gln	TCA Ser 330	GCC Ala	AAT Asn	TTC Phe	TAC Tyr	AAG Lys 335	CAT His	1008
TGG Trp	ATC Ile	TCA Ser	ACA Thr 340	GTA Val	GCA Ala	GGA Gly	CAC His	TGT Cys 345	GGA Gly	AAC Asn	CCT Pro	ATG Met	GTT Val 350	TCG Ser	ACT Thr	1056
AAA Lys	GAT Asp	GGA Gly 355	TTT Phe	ATT Ile	GTA Val	GGT Gly	ATC Ile 360	CAC His	AGT Ser	CTT Leu	GCT Ala	TCA Ser 365	TTG Leu	ACA Thr	GGC Gly	1104
GAC Asp	GTT Val 370	AAC Asn	ATC Ile	TTC Phe	ACA Thr	AGC Ser 375	TTT Phe	CCG Pro	CCG Pro	CAG Gln	TTT Phe 380	GAG Glu	AAC Asn	AAA Lys	TAT Tyr	1152
CTA Leu 385	CAG Gln	AAG Lys	CTC Leu	AGT Ser	GAA Glu 390	CAC His	ACA Thr	TGG Trp	TGT Cys	AGT Ser 395	GGA Gly	TGG Trp	AAA Lys	CTA Leu	AAT Asn 400	1200
CTT Leu	GGA Gly	AAG Lys	ATT Ile	AGT Ser 405	TGG Trp	GGT Gly	GGA Gly	ATC Ile 410	AAC Asn	ATT Ile	GTG Val	GAG Glu	GAT Asp	GCA Ala 415	CCT Pro	1248

Phe	Glu	Ser	Leu	Asn	Arg	Ile	Ser	Gly	Leu	Arg	Asp	Tyr	Asn	Pro	Ile	195	200	205
Ser	Gln	Asn	Val	Cys	Leu	Leu	Thr	Asn	Glu	Ser	Glu	Gly	His	Arg	Glu	210	215	220
Lys	Met	Phe	Gly	Ile	Gly	Tyr	Gly	Ser	Val	Ile	Ile	Thr	Asn	Gln	His	225	230	235
Leu	Phe	Arg	Arg	Asn	Asn	Gly	Glu	Leu	Ser	Ile	Gln	Ser	Lys	His	Gly	245	250	255
Tyr	Phe	Arg	Cys	Arg	Asn	Thr	Thr	Ser	Leu	Lys	Met	Leu	Pro	Leu	Glu	260	265	270
Gly	His	Asp	Ile	Leu	Leu	Ile	Gln	Leu	Pro	Arg	Asp	Phe	Pro	Val	Phe	275	280	285
Pro	Gln	Lys	Ile	Arg	Phe	Arg	Glu	Pro	Arg	Val	Asp	Asp	Lys	Ile	Val	290	295	300
Leu	Val	Ser	Thr	Asn	Phe	Gln	Glu	Lys	Ser	Ser	Ser	Ser	Thr	Val	Ser	305	310	315
Glu	Ser	Ser	Asn	Ile	Ser	Arg	Val	Gln	Ser	Ala	Asn	Phe	Tyr	Lys	His	325	330	335
Trp	Ile	Ser	Thr	Val	Ala	Gly	His	Cys	Gly	Asn	Pro	Met	Val	Ser	Thr	340	345	350
Lys	Asp	Gly	Phe	Ile	Val	Gly	Ile	His	Ser	Leu	Ala	Ser	Leu	Thr	Gly	355	360	365
Asp	Val	Asn	Ile	Phe	Thr	Ser	Phe	Pro	Pro	Gln	Phe	Glu	Asn	Lys	Tyr	370	375	380
Leu	Gln	Lys	Leu	Ser	Glu	His	Thr	Trp	Cys	Ser	Gly	Trp	Lys	Leu	Asn	385	390	395
Leu	Gly	Lys	Ile	Ser	Trp	Gly	Gly	Ile	Asn	Ile	Val	Glu	Asp	Ala	Pro	405	410	415
Glu	Glu	Pro	Phe	Ile	Thr	Ser	Lys	Met	Ala	Ser	Leu	Leu	Ser	Asp	Leu	420	425	430
Asn	Cys	Ser	Phe	Gln	Ala	Ser	Ala									435	440	

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GTCCATGGGG AAAAGTAAGA GAACA

25

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACTCTGAGAC CGTGCTCGAG

20

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

AGGAAAAGAG TTCCTCGAGC

20

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AATTGTTTCAT TCCAAGCACC TGGGCCACCA CCTGGC

36

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 36 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCCAGGTGGT GCGCCAGGTG CTTGGAATGA ACAATT

36

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTGTCAGCAC ACCTGGGAGC TG TAGAGCTC

30

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Ala Pro Gly Pro Pro Pro Gly
1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Pro Gly Pro Pro Pro Gly Pro
 1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1650 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens
 (H) CELL LINE: KM-102

(vii) IMMEDIATE SOURCE:
 (B) CLONE: KM31-7

(ix) FEATURE:
 (A) NAME/KEY: CDS
 (B) LOCATION: 1..1647
 (D) OTHER INFORMATION:

(ix) FEATURE:
 (A) NAME/KEY: mat_peptide
 (B) LOCATION: 70..1647
 (D) OTHER INFORMATION:

(ix) FEATURE:
 (A) NAME/KEY: sig_peptide
 (B) LOCATION: 1..69
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG TCA TGT GAG GAC GGT CGG GCC CTG GAA GGA ACG CTC TCG GAA TTG	48
Met Ser Cys Glu Asp Gly Arg Ala Leu Glu Gly Thr Leu Ser Glu Leu	
-23 -20 -15 -10	
GCC GCG GAA ACC GAT CTG CCC GTT GTG TTT GTG AAA CAG AGA AAG ATA	96
Ala Ala Glu Thr Asp Leu Pro Val Val Phe Val Lys Gln Arg Lys Ile	
-5 1 5	
GGC GGC CAT GGT CCA ACC TTG AAG GCT TAT CAG GAG GGC AGA CTT CAA	144
Gly Gly His Gly Pro Thr Leu Lys Ala Tyr Gln Glu Gly Arg Leu Gln	
10 15 20 25	

AAG CTA CTA AAA ATG AAC GGC CCT GAA GAT CTT CCC AAG TCC TAT GAC	192
Lys Leu Leu Lys Met Asn Gly Pro Glu Asp Leu Pro Lys Ser Tyr Asp	
30 35 40	
TAT GAC CTT ATC ATC ATT GGA GGT GGC TCA GGA GGT CTG GCA GCT GCT	240
Tyr Asp Leu Ile Ile Ile Gly Gly Gly Ser Gly Gly Leu Ala Ala Ala	
45 50 55	
AAG GAG GCA GCC CAA TAT GGC AAG AAG GTG ATG GTC CTG GAC TTT GTC	288
Lys Glu Ala Ala Gln Tyr Gly Lys Lys Val Met Val Leu Asp Phe Val	
60 65 70	
ACT CCC ACC CCT CTT GGA ACT AGA TGG GGT CTT GGA GGA ACA TGT GTG	336
Thr Pro Thr Pro Leu Gly Thr Arg Trp Gly Leu Gly Gly Thr Cys Val	
75 80 85	
AAT GTG GGT TGC ATA CCT AAA AAA CTG ATG CAT CAA GCA GCT TTG TTA	384
Asn Val Gly Cys Ile Pro Lys Lys Leu Met His Gln Ala Ala Leu Leu	
90 95 100 105	
GGA CAA GCC CTG CAA GAC TCT CGA AAT TAT GGA TGG AAA GTC GAG GAG	432
Gly Gln Ala Leu Gln Asp Ser Arg Asn Tyr Gly Trp Lys Val Glu Glu	
110 115 120	
ACA GTT AAG CAT GAT TGG GAC AGA ATG ATA GAA GCT GTA CAG AAT CAC	480
Thr Val Lys His Asp Trp Asp Arg Met Ile Glu Ala Val Gln Asn His	
125 130 135	
ATT GGC TCT TTG AAT TGG GGC TAC CGA GTA GCT CTG CGG GAG AAA AAA	528
Ile Gly Ser Leu Asn Trp Gly Tyr Arg Val Ala Leu Arg Glu Lys Lys	
140 145 150	
GTC GTC TAT GAG AAT GCT TAT GGG CAA TTT ATT GGT CCT CAC AGG ATT	576
Val Val Tyr Glu Asn Ala Tyr Gly Gln Phe Ile Gly Pro His Arg Ile	
155 160 165	
AAG GCA ACA AAT AAT AAA GGC AAA GAA AAA ATT TAT TCA GCA GAG AGA	624
Lys Ala Thr Asn Asn Lys Gly Lys Glu Lys Ile Tyr Ser Ala Glu Arg	
170 175 180 185	
TTT CTC ATT GCC ACT GGT GAA AGA CCA CGT TAC TTG GGC ATC CCT GGT	672
Phe Leu Ile Ala Thr Gly Glu Arg Pro Arg Tyr Leu Gly Ile Pro Gly	
190 195 200	
GAC AAA GAA TAC TGC ATC AGC AGT GAT GAT CTT TTC TCC TTG CCT TAC	720
Asp Lys Glu Tyr Cys Ile Ser Ser Asp Asp Leu Phe Ser Leu Pro Tyr	
205 210 215	
TGC CCG GGT AAG ACC CTG GTT GTT GGA GCA TCC TAT GTC GCT TTG GAG	768
Cys Pro Gly Lys Thr Leu Val Val Gly Ala Ser Tyr Val Ala Leu Glu	
220 225 230	
TGC GCT GGA TTT CTT GCT GGT ATT GGT TTA GAC GTC ACT GTT ATG GTT	816
Cys Ala Gly Phe Leu Ala Gly Ile Gly Leu Asp Val Thr Val Met Val	
235 240 245	
AGG TCC ATT CTT CTT AGA GGA TTT GAC CAG GAC ATG GCC AAC AAA ATT	864
Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile	
250 255 260 265	
GGT GAA CAC ATG GAA GAA CAT GGC ATC AAG TTT ATA AGA CAG TTC GTA	912
Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val	
270 275 280	

CCA	ATT	AAA	GTT	GAA	CAA	ATT	GAA	GCA	GGG	ACA	CCA	GGC	CGA	CTC	AGA	960
Pro	Ile	Lys	Val	Glu	Gln	Ile	Glu	Ala	Gly	Thr	Pro	Gly	Arg	Leu	Arg	
			285					290					295			
GTA	GTA	GCT	CAG	TCC	ACC	AAT	AGT	GAG	GAA	ATC	ATT	GAA	GGA	GAA	TAT	1008
Val	Val	Ala	Gln	Ser	Thr	Asn	Ser	Glu	Glu	Ile	Ile	Glu	Gly	Glu	Tyr	
			300				305					310				
AAT	ACG	GTG	ATG	CTG	GCA	ATA	GGA	AGA	GAT	GCT	TGC	ACA	AGA	AAA	ATT	1056
Asn	Thr	Val	Met	Leu	Ala	Ile	Gly	Arg	Asp	Ala	Cys	Thr	Arg	Lys	Ile	
			315			320					325					
GGC	TTA	GAA	ACC	GTA	GGG	GTG	AAG	ATA	AAT	GAA	AAG	ACT	GGA	AAA	ATA	1104
Gly	Leu	Glu	Thr	Val	Gly	Val	Lys	Ile	Asn	Glu	Lys	Thr	Gly	Lys	Ile	
					335					340					345	
CCT	GTC	ACA	GAT	GAA	GAA	CAG	ACC	AAT	GTG	CCT	TAC	ATC	TAT	GCC	ATT	1152
Pro	Val	Thr	Asp	Glu	Glu	Gln	Thr	Asn	Val	Pro	Tyr	Ile	Tyr	Ala	Ile	
				350					355					360		
GGC	GAT	ATA	TTG	GAG	GAT	AAG	GTG	GAG	CTC	ACC	CCA	GTT	GCA	ATC	CAG	1200
Gly	Asp	Ile	Leu	Glu	Asp	Lys	Val	Glu	Leu	Thr	Pro	Val	Ala	Ile	Gln	
			365				370						375			
GCA	GGA	AGA	TTG	CTG	GCT	CAG	AGG	CTC	TAT	GCA	GGT	TCC	ACT	GTC	AAG	1248
Ala	Gly	Arg	Leu	Leu	Ala	Gln	Arg	Leu	Tyr	Ala	Gly	Ser	Thr	Val	Lys	
			380				385					390				
TGT	GAC	TAT	GAA	AAT	GTT	CCA	ACC	ACT	GTA	TTT	ACT	CCT	TTG	GAA	TAT	1296
Cys	Asp	Tyr	Glu	Asn	Val	Pro	Thr	Thr	Val	Phe	Thr	Pro	Leu	Glu	Tyr	
			395			400					405					
GGT	GCT	TGT	GGC	CTT	TCT	GAG	GAG	AAA	GCT	GTG	GAG	AAG	TTT	GGG	GAA	1344
Gly	Ala	Cys	Gly	Leu	Ser	Glu	Glu	Lys	Ala	Val	Glu	Lys	Phe	Gly	Glu	
					415				420						425	
GAA	AAT	ATT	GAG	GTT	TAC	CAT	AGT	TAC	TTT	TGG	CCA	TTG	GAA	TGG	ACG	1392
Glu	Asn	Ile	Glu	Val	Tyr	His	Ser	Tyr	Phe	Trp	Pro	Leu	Glu	Trp	Thr	
				430					435					440		
ATT	CCG	TCA	AGA	GAT	AAC	AAC	AAA	TGT	TAT	GCA	AAA	ATA	ATC	TGT	AAT	1440
Ile	Pro	Ser	Arg	Asp	Asn	Asn	Lys	Cys	Tyr	Ala	Lys	Ile	Ile	Cys	Asn	
			445					450					455			
ACT	AAA	GAC	AAT	GAA	CGT	GTT	GTG	GGC	TTT	CAC	GTA	CTG	GGT	CCA	AAT	1488
Thr	Lys	Asp	Asn	Glu	Arg	Val	Val	Gly	Phe	His	Val	Leu	Gly	Pro	Asn	
				460			465					470				
GCT	GGA	GAA	GTT	ACA	CAA	GGC	TTT	GCA	GCT	GCG	CTC	AAA	TGT	GGA	CTG	1536
Ala	Gly	Glu	Val	Thr	Gln	Gly	Phe	Ala	Ala	Ala	Leu	Lys	Cys	Gly	Leu	
						480					485					
ACC	AAA	AAG	CAG	CTG	GAC	AGC	ACA									

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 549 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ser	Cys	Glu	Asp	Gly	Arg	Ala	Leu	Glu	Gly	Thr	Leu	Ser	Glu	Leu	
-23			-20					-15						-10		
Ala	Ala	Glu	Thr	Asp	Leu	Pro	Val	Val	Phe	Val	Lys	Gln	Arg	Lys	Ile	
		-5					1				5					
Gly	Gly	His	Gly	Pro	Thr	Leu	Lys	Ala	Tyr	Gln	Glu	Gly	Arg	Leu	Gln	
10					15					20					25	
Lys	Leu	Leu	Lys	Met	Asn	Gly	Pro	Glu	Asp	Leu	Pro	Lys	Ser	Tyr	Asp	
				30					35						40	
Tyr	Asp	Leu	Ile	Ile	Ile	Gly	Gly	Gly	Ser	Gly	Gly	Leu	Ala	Ala	Ala	
			45					50					55			
Lys	Glu	Ala	Ala	Gln	Tyr	Gly	Lys	Lys	Val	Met	Val	Leu	Asp	Phe	Val	
		60					65					70				
Thr	Pro	Thr	Pro	Leu	Gly	Thr	Arg	Trp	Gly	Leu	Gly	Gly	Thr	Cys	Val	
		75				80					85					
Asn	Val	Gly	Cys	Ile	Pro	Lys	Lys	Leu	Met	His	Gln	Ala	Ala	Leu	Leu	
90					95					100					105	
Gly	Gln	Ala	Leu	Gln	Asp	Ser	Arg	Asn	Tyr	Gly	Trp	Lys	Val	Glu	Glu	
				110					115					120		
Thr	Val	Lys	His	Asp	Trp	Asp	Arg	Met	Ile	Glu	Ala	Val	Gln	Asn	His	
			125					130					135			
Ile	Gly	Ser	Leu	Asn	Trp	Gly	Tyr	Arg	Val	Ala	Leu	Arg	Glu	Lys	Lys	
			140				145					150				
Val	Val	Tyr	Glu	Asn	Ala	Tyr	Gly	Gln	Phe	Ile	Gly	Pro	His	Arg	Ile	
		155				160					165					
Lys	Ala	Thr	Asn	Asn	Lys	Gly	Lys	Glu	Lys	Ile	Tyr	Ser	Ala	Glu	Arg	
170					175					180					185	
Phe	Leu	Ile	Ala	Thr	Gly	Glu	Arg	Pro	Arg	Tyr	Leu	Gly	Ile	Pro	Gly	
				190					195					200		
Asp	Lys	Glu	Tyr	Cys	Ile	Ser	Ser	Asp	Asp	Leu	Phe	Ser	Leu	Pro	Tyr	
			205					210					215			
Cys	Pro	Gly	Lys	Thr	Leu	Val	Val	Gly	Ala	Ser	Tyr	Val	Ala	Leu	Glu	
		220					225					230				
Cys	Ala	Gly	Phe	Leu	Ala	Gly	Ile	Gly	Leu	Asp	Val	Thr	Val	Met	Val	
		235				240						245				

Arg Ser Ile Leu Leu Arg Gly Phe Asp Gln Asp Met Ala Asn Lys Ile
 250 255 260 265
 Gly Glu His Met Glu Glu His Gly Ile Lys Phe Ile Arg Gln Phe Val
 270 275 280
 Pro Ile Lys Val Glu Gln Ile Glu Ala Gly Thr Pro Gly Arg Leu Arg
 285 290 295
 Val Val Ala Gln Ser Thr Asn Ser Glu Glu Ile Ile Glu Gly Glu Tyr
 300 305 310
 Asn Thr Val Met Leu Ala Ile Gly Arg Asp Ala Cys Thr Arg Lys Ile
 315 320 325
 Gly Leu Glu Thr Val Gly Val Lys Ile Asn Glu Lys Thr Gly Lys Ile
 330 335 340 345
 Pro Val Thr Asp Glu Glu Gln Thr Asn Val Pro Tyr Ile Tyr Ala Ile
 350 355 360
 Gly Asp Ile Leu Glu Asp Lys Val Glu Leu Thr Pro Val Ala Ile Gln
 365 370 375
 Ala Gly Arg Leu Leu Ala Gln Arg Leu Tyr Ala Gly Ser Thr Val Lys
 380 385 390
 Cys Asp Tyr Glu Asn Val Pro Thr Thr Val Phe Thr Pro Leu Glu Tyr
 395 400 405
 Gly Ala Cys Gly Leu Ser Glu Glu Lys Ala Val Glu Lys Phe Gly Glu
 410 415 420 425
 Glu Asn Ile Glu Val Tyr His Ser Tyr Phe Trp Pro Leu Glu Trp Thr
 430 435 440
 Ile Pro Ser Arg Asp Asn Asn Lys Cys Tyr Ala Lys Ile Ile Cys Asn
 445 450 455
 Thr Lys Asp Asn Glu Arg Val Val Gly Phe His Val Leu Gly Pro Asn
 460 465 470
 Ala Gly Glu Val Thr Gln Gly Phe Ala Ala Ala Leu Lys Cys Gly Leu
 475 480 485
 Thr Lys Lys Gln Leu Asp Ser Thr Ile Gly Ile His Pro Val Cys Ala
 490 495 500 505
 Glu Val Phe Thr Thr Leu Ser Val Thr Lys Arg Ser Gly Ala Ser Ile
 510 515 520
 Leu Gln Ala Gly Cys
 525

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TAAATAAATA AATAA

15

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 66 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTAGCGCTCT GGGGCAAGCA TCCTCCAGGC TGGCTGCCAC CACCACCACC ACCACTGATC

60

TAGACT

66

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GGTCAGCACA AATTTCCA

18

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

AAACACAAC TGAATGAAC AATT

24

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

TCATTCCAAG TTGTGTTTGT GAAA

24

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid, synthetic DNA

(iii) HYPOTHETICAL: N

(iv) ANTI-SENSE: N

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CATAGGATGC TCCAACAA

18

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asn Cys Ser Phe Gln Xaa

1

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